



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/829,504
Source: 1Fwo
Date Processed by STIC: 4/30/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/829,504</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input checked="" type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) <u>38-49</u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/829,504

DATE: 04/30/2004
TIME: 15:26:36

Input Set : A:\23239-558A.ST25.txt
Output Set: N:\CRF4\04122004\J829504.raw

3 <110> APPLICANT: Epstein, David
 4 Stanton, Martin
 5 DeSouza, Errol
 6 Wilson, Chuck
 7 Grate, Dilara
 8 McCauley, Tom
 9 Diener, John
 11 <120> TITLE OF INVENTION: Stabilized Aptamers to Platelet Derived Growth Factor and
 Their
 12 Use as Oncology Therapeutics
 14 <130> FILE REFERENCE: 23239-558A (ARC-58A)
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/829,504
 17 <141> CURRENT FILING DATE: 2004-04-21
 19 <160> NUMBER OF SEQ ID NOS: 98
 21 <170> SOFTWARE: PatentIn version 3.2

ppr 1-4

ERRORED SEQUENCES

835 <210> SEQ ID NO: 38
 836 <211> LENGTH: 0
 837 <212> TYPE: DNA
 C--> 838 <213> ORGANISM: Artificial:aptamer
 W--> 840 <220> FEATURE:
 W--> 840 <223> OTHER INFORMATION:
 W--> 840 <400> 38
 E--> 841 000
 844 <210> SEQ ID NO: 39
 845 <211> LENGTH: 0
 846 <212> TYPE: DNA
 C--> 847 <213> ORGANISM: Artificial:aptamer
 W--> 849 <220> FEATURE:
 W--> 849 <223> OTHER INFORMATION:
 W--> 849 <400> 39
 E--> 850 000
 853 <210> SEQ ID NO: 40
 854 <211> LENGTH: 0
 855 <212> TYPE: DNA
 C--> 856 <213> ORGANISM: Artificial:aptamer
 W--> 858 <220> FEATURE:
 W--> 858 <223> OTHER INFORMATION:
 W--> 858 <400> 40
 E--> 859 000
 862 <210> SEQ ID NO: 41

Does Not Comply
Connected Diskette Needed
 If this is an intentionally
 skipped sequence, show
 only
 delete
 ↗
 <210> 38
 <400> 38
 000
 (see
 item 8
 on Error
 Summary
 Sheet)

RAW SEQUENCE LISTING
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DATE: 04/30/2004
TIME: 15:26:36

Input Set : A:\23239-558A.ST25.txt
Output Set: N:\CRF4\04122004\J829504.raw

863 <211> LENGTH: 0
864 <212> TYPE: DNA
C--> 865 <213> ORGANISM: Artificial:aptamer
W--> 867 <220> FEATURE:
W--> 867 <223> OTHER INFORMATION:
W--> 867 <400> 41
E--> 868 000
871 <210> SEQ ID NO: 42
872 <211> LENGTH: 0
873 <212> TYPE: DNA
C--> 874 <213> ORGANISM: Artificial:aptamer
W--> 876 <220> FEATURE:
W--> 876 <223> OTHER INFORMATION:
W--> 876 <400> 42
E--> 877 000
880 <210> SEQ ID NO: 43
881 <211> LENGTH: 0
882 <212> TYPE: DNA
C--> 883 <213> ORGANISM: Artificial:aptamer
W--> 885 <220> FEATURE:
W--> 885 <223> OTHER INFORMATION:
W--> 885 <400> 43
E--> 886 000
889 <210> SEQ ID NO: 44
890 <211> LENGTH: 0
891 <212> TYPE: DNA
C--> 892 <213> ORGANISM: Artificial:aptamer
W--> 894 <220> FEATURE:
W--> 894 <223> OTHER INFORMATION:
W--> 894 <400> 44
E--> 895 000
898 <210> SEQ ID NO: 45
899 <211> LENGTH: 0
900 <212> TYPE: DNA
C--> 901 <213> ORGANISM: Artificial:aptamer
W--> 903 <220> FEATURE:
W--> 903 <223> OTHER INFORMATION:
W--> 903 <400> 45
E--> 904 000
907 <210> SEQ ID NO: 46
908 <211> LENGTH: 0
909 <212> TYPE: DNA
C--> 910 <213> ORGANISM: Artificial:aptamer
W--> 912 <220> FEATURE:
W--> 912 <223> OTHER INFORMATION:
W--> 912 <400> 46
E--> 913 000
916 <210> SEQ ID NO: 47
917 <211> LENGTH: 0

delete

delete

delete

delete

delete

delete

delete

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/829,504

DATE: 04/30/2004
TIME: 15:26:36

Input Set : A:\23239-558A.ST25.txt
Output Set: N:\CRF4\04122004\J829504.raw

918 <212> TYPE: DNA
C--> 919 <213> ORGANISM: Artificial:aptamer
W--> 921 <220> FEATURE:
W--> 921 <223> OTHER INFORMATION:
W--> 921 <400> 47
E--> 922 000
925 <210> SEQ ID NO: 48
926 <211> LENGTH: 0
927 <212> TYPE: DNA
C--> 928 <213> ORGANISM: Artificial:aptamer
W--> 930 <220> FEATURE:
W--> 930 <223> OTHER INFORMATION:
W--> 930 <400> 48
E--> 931 000
934 <210> SEQ ID NO: 49
935 <211> LENGTH: 0
936 <212> TYPE: DNA
C--> 937 <213> ORGANISM: Artificial:aptamer
W--> 939 <220> FEATURE:
W--> 939 <223> OTHER INFORMATION:
W--> 939 <400> 49
E--> 940 000

delete

delete

delete

see p. 4 for more errors

10/829,504 4

<210> 1
<211> 9
<212> DNA
<213> Artificial aptamer

<220>
<223> ←
<220>

<221> modified_base
<222> (6)..(6)
<223> 2'-Fluoro-Uracil

<220>
<221> modified_base
<222> (6)..(6)
<223> *2'-Fluoro-Uracil

<220>
<221> modified_base
<222> (8)..(8)
<223> 2'-Fluoro-Cytosine

<220>
<221> modified_base
<222> (9)..(9)
<223> gm

<400> 1
caggcuacg

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

delete colon:

do not show explanation for
Artificial Sequence on 2137

line. insert a <220>,
a <223>, and

move
explanation
to 2237
line.

delete - already shown above

Explanation of
Artificial Sequence
Must give Source
of genetic material.

This
error
appears
throughout
Sequence Listing.

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/829,504

DATE: 04/30/2004
TIME: 15:26:37

Input Set : A:\23239-558A.ST25.txt
Output Set: N:\CRF4\04122004\J829504.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:26 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:56 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:91 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:116 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:156 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:191 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:216 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:326 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:328 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:328 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:328 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:328
L:335 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:445 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:545 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:547 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:547 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:547 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:547
L:554 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:569 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:584 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:599 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:614 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:629 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:644 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:659 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:674 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:676 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:676 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:676 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:676
L:683 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:685 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:685 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:685 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:685
L:692 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:694 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:694 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:694 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:694
L:703 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:705 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:705 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence

L:705 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:705
L:712 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:714 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:714 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:714 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:714
L:721 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:723 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/829,504

DATE: 04/30/2004
TIME: 15:26:37

Input Set : A:\23239-558A.ST25.txt
Output Set: N:\CRF4\04122004\J829504.raw

L:723 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:723 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:723
L:730 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:732 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:732 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:732 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:732
L:739 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:741 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:741 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:741 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:741
L:748 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:750 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:750 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:750 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:750
L:757 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:759 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:759 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:759 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:759
L:766 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:30, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:30, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:768
L:775 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:777 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial Sequence
L:777 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial Sequence
L:777 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:777
L:784 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:786 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial Sequence
L:786 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial Sequence
L:786 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:786
L:793 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:795 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:Artificial Sequence
L:795 M:258 W: Mandatory Feature missing, <223> Tag not founfd for SEQ#:33, <213>
ORGANISM:Artificial Sequence
L:795 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:795
L:802 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:804 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:34, <213>

ORGANISM:Artificial Sequence
L:804 M:258 W: Mandatory Feature missing, <213> Tag not found for SEQ#:34, <213>
ORGANISM:Artificial Sequence
L:811 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:829 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:838 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:841 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:841 M:301 E: (44) No Sequence Data was Shown, SEQ ID:38
L:847 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:850 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:850 M:301 E: (44) No Sequence Data was Shown, SEQ ID:39
L:856 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:859 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:859 M:301 E: (44) No Sequence Data was Shown, SEQ ID:40

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Input Set : A:\23239-558A.ST25.txt
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L:865 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:868 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:868 M:301 E: (44) No Sequence Data was Shown, SEQ ID:41
L:874 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:877 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:877 M:301 E: (44) No Sequence Data was Shown, SEQ ID:42
L:883 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:886 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:886 M:301 E: (44) No Sequence Data was Shown, SEQ ID:43
L:892 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:895 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:895 M:301 E: (44) No Sequence Data was Shown, SEQ ID:44
L:901 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:904 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:904 M:301 E: (44) No Sequence Data was Shown, SEQ ID:45
L:910 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:913 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:913 M:301 E: (44) No Sequence Data was Shown, SEQ ID:46
L:919 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:922 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:922 M:301 E: (44) No Sequence Data was Shown, SEQ ID:47
L:928 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
L:931 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:931 M:301 E: (44) No Sequence Data was Shown, SEQ ID:48
L:937 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:49
L:940 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:940 M:301 E: (44) No Sequence Data was Shown, SEQ ID:49
L:946 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:1863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
M:341 Repeated in SeqNo=91